

diversification demonstrates a need for studies into how distinct taxonomic groups contribute to microbiome function.

Synthetic microbial communities can be used to systematically query natural microbiome processes. Bai *et al.* introduced synthetic communities of 188 and 218 representative isolates from root (or soil) and leaf communities, respectively, onto gnotobiotic *Arabidopsis* plants — plants that were microorganism-free before inoculation with known microorganisms. They then evaluated the communities that assembled by sequencing genes that help to identify the taxa (the 16S ribosomal RNA genes). These synthetic communities yielded assemblages on gnotobiotic plants that had consistent compositions, showing reproducibility in microbiome assembly processes; moreover, their composition resembled the native bacterial microbiomes found on wild *Arabidopsis* plants. Surprisingly, the resulting communities were not influenced by the relative proportion of the applied strains, indicating that community assembly is a robust process.

The synthetic communities were also instrumental in teasing apart two of the drivers of community assembly on *Arabidopsis* leaves: the source of the isolates (roots or leaves), and their arrival through the air or the soil. These findings demonstrate how synthetic communities can serve as windows on the origins and development of the bacterial component of plant microbiomes.

We are at a crucial juncture in microbiome research, transitioning from cataloguing microbes and genes to executing hypothesis-driven experiments. Bai and colleagues have provided resources that will speed this transition for plant research, including a

large culture collection, complex synthetic communities with sequenced genomes and a gnotobiotic reconstitution system. Together, these resources enable recapitulation of the assembly of native bacterial communities on *Arabidopsis* plants, facilitating studies that provide ecologically relevant answers to questions about the establishment, dynamics, resilience, function and evolution of plant microbiomes. The mechanistic understanding derived from these synthetic communities is an excellent step on the road to understanding how the sustained health and productivity of our agricultural and natural systems are influenced by plant microbiomes and, more broadly, by phytobiomes — the networks of bacteria, fungi, oomycetes, viruses, nematodes, insects and other animals that affect plants. ■

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CLIMATE SCIENCE

A history of Greenland's ice loss

Aerial photographs, remote-sensing observations and geological evidence together provide a reconstruction of mass loss from the Greenland Ice Sheet since 1900 — a great resource for climate scientists. SEE LETTER P.396

BEATA M. CSATHO

Loss of ice-sheet mass is a major contributor to current sea-level rise, and is expected to continue as global warming proceeds¹. Detailed reconstructions of changes in the Greenland and Antarctic ice sheets over the past few decades are available, based on remotely sensed data. But extending this record further into the past poses a

big problem because of the lack of systematic monitoring of changes in ice-sheet elevations. On page 396 of this issue, Kjeldsen *et al.*² present the first observation-based estimate of mass loss from the Greenland Ice Sheet from the end of the nineteenth century, when it began to retreat from its maximum extent achieved during the Little Ice Age (LIA), to the present day. Their findings show how the reconstruction of past ice-sheet changes



Figure 1 | The Upernavik Ice Stream in northwest Greenland. This glacier is one of many that drain the Greenland Ice Sheet into the sea. A trimline — distinguished by differently coloured rock above and below the line — is visible in the nearby hill, and indicates the maximum extent of ice during the Little Ice Age (LIA). Kjeldsen *et al.*² report a reconstruction of mass loss from the Greenland Ice Sheet since 1900, the end of the LIA.

helps to account for sources of sea-level rise and improves our understanding of the major processes controlling ice-sheet mass loss.

Historical photographs of ice sheets provide long-term context for mass loss by enabling measurements of their surface elevations and extent before satellites were used for remote sensing. Moreover, they facilitate the accurate mapping of glacial geomorphic features such as vegetation trimlines (Fig. 1) and moraines, which mark the highest extent of the ice sheet during the LIA in the case of the Greenland Ice Sheet. A treasure trove of aerial photographs of Greenland has been extensively used for many years³, but because of the difficulty in obtaining accurate surface-elevation measurements from historical photographs, a detailed timeline of mass loss was reconstructed only for the largest glaciers^{4,5}.

To estimate the mass-balance history of the Greenland Ice Sheet — the time course of differences between mass gained by snow accumulation and that lost by melting and calving of icebergs — since the LIA, Kjeldsen *et al.* began by reprocessing images taken by the comprehensive Greenland aerial photography survey during 1978–87. They used modern photogrammetric methods to derive high-resolution, accurate digital elevation models (DEMs) depicting the ice-sheet surface at the sheet's margins during the survey period. They also reconstructed the ice-sheet margins during the LIA in three dimensions by mapping vegetation trimlines and glacial moraines. Taken together with laser-altimetry measurements from 2003 to 2010, these analyses enabled the authors to determine elevation changes for three different epochs since the 1900s.

The results show that the Greenland Ice

Sheet contributed substantially to sea-level rise throughout the twentieth century, providing at least 25 ± 9.4 millimetres of the total global mean rise. Furthermore, rates of mass loss during 2003–10 were twice those during the twentieth century, mostly because of increasing water runoff from the surface, whereas discharge through iceberg calving has remained essentially the same since the LIA.

Kjeldsen and colleagues also report a large spatial variation in ice-sheet changes, indicating that the sheet's response to climate forcing is modulated by local geometric factors such as the topography of the underlying bed and the sizes of the drainage basins of individual glaciers. The striking similarity between the elevation-change patterns during the different epochs suggests that local controls act similarly on both decadal and centennial timescales.

The authors' discovery of a large mass loss, which averaged 75 gigatonnes per year (equivalent to a sea-level rise of 0.21 mm yr^{-1}) during the twentieth century, emphasizes the need for improvements to the record of ice-sheet changes before the start of detailed remote-sensing measurements in the 1990s. Existing long-term records are usually based on time series of the positions of ice-sheet margins, but such records can be misleading for glaciers that flow into the ocean, whose floating termini can advance or retreat without any substantial changes farther up-glacier. Furthermore, only repeated elevation measurements allow the quantification of mass loss that is necessary to estimate contributions to sea-level rise. Kjeldsen and co-workers' results provide an excellent framework for selecting regions that represent different long-term mass-loss patterns for further detailed studies.

A crucial objective of those studies should be to examine the stability of the Greenland Ice Sheet between 1960 and 1990. It has been assumed that this ice sheet was in equilibrium during this period, and so calculated changes in its surface mass-balance relative to the average during 1960–90 are used to work out whether recent ice-sheet surface losses are anomalous⁶. Kjeldsen *et al.* challenge this assumption by arguing that it contradicts the long-term persistent mass loss detected in their study. However, the temporal sampling of their study is not sufficiently detailed to rule out the possibility that a near-steady-state condition existed following the warm period that occurred in the 1930s and 1940s.

The rich archive of historical stereo aerial photographs of Greenland includes: systematic surveys taken during the 1930s that were used to generate 1:250,000 scale topographic maps; oblique aerial photographs taken by the US Air Force for reconnaissance during the Second World War using a Trimetrogon camera (which also enable topographic information to be determined); and repeat surveys of the catchment basins of all major outlet glaciers around the Jakobshavn Isbræ during 1957–58 and in 1964, taken as part of the International Glaciological Expeditions to Greenland. Moreover, high-resolution stereo images collected by US intelligence satellites are available from the 1960s and 1970s. If all of these were combined with more-recent satellite observations, then a comprehensive record of long-term surface elevation, positions of calving fronts and ice margins, and ice-velocity changes could be obtained. This could be used to assess the implications of recent changes in the context of climate change and to provide input for modelling studies.

In the meantime, the authors' reconstruction will help to improve numerical models — by providing a time series of changes at ice sheet margins for the whole Greenland Ice Sheet during the twentieth century, suitable for validating models. Although the extensive spatial overlap of laser altimetry and DEMs derived from stereo photogrammetry along the ice-sheet margins provides robust and accurate change detection in these regions between the 1980s and the present, further research — particularly the use of more-realistic ice-sheet models — is needed to derive accurate elevations within the interior of the ice sheet before the start of laser-altimetry observations in the 1990s. Improving the accuracy of past elevation reconstructions would result in better estimates of long-term mass-balance changes.

Finally, once the timing of equilibrium conditions for the Greenland Ice Sheet is verified, a detailed reconstruction for that period could serve as a steady-state ice-sheet surface for initializing ice-sheet models. Establishing such a steady-state surface is a prerequisite for deriving projections of future ice-sheet evolution

that are more credible than currently available projections. ■

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In retrospect

Twenty-five years of the sex-determining gene

The discovery that the gene *SRY* on the mammalian Y chromosome drives testis development marked a turning point in the decades-long quest to understand the genetic underpinnings and evolution of sex determination.

JENNIFER A. MARSHALL GRAVES

It has long been known that a testis-determining factor (TDF) on the Y chromosome kick-starts testis development in humans and other mammals. The testes make hormones, and these hormones make the embryo male. Twenty-five years ago, Sinclair *et al.*¹ reported in *Nature* that TDF was the gene *SRY*. This discovery opened up the surprisingly intricate genetic pathway that determines whether a baby is born a boy or a girl. It also led to an understanding of how genes on the Y chromosome evolved, and of the impact of this key evolutionary event.

Until the 1980s, there was no viable candidate sex-determining gene. Just where was TDF located? What kind of product did it encode? What did it do? During the 1980s, the position of TDF was narrowed down to a small region on the short arm of the Y chromosome, when it was found that some males had XX chromosomes that harboured a small piece of the Y, whereas some females had XY chromosomes that lacked bits of the Y — these added and deleted regions of Y were assumed to contain the TDF sequence. The race was then on to find TDF.

In 1987, the geneticist David Page and his associates² identified the first coding gene on the human Y, called *ZFY*. The gene looked like a winning candidate: it was in the right place; it was expressed in the testis; and it was evolutionarily conserved in other placental mammals, such as monkeys, mice, dogs and horses. But in 1988, PhD students in my laboratory³, Andrew Sinclair and Jamie Foster, mapped *ZFY* to a non-sex chromosome (an autosome) in marsupials, which are a separate branch of mammals. A few months later, it

was found⁴ that, although *ZFY* is expressed in mouse sperm precursors, it is absent from the other cells of the testis, where a true TDF must be expressed to exert a sex-determining effect.

Sinclair joined a renewed hunt for human TDF in the laboratory of geneticist Peter Goodfellow, using DNA from XY males that had even smaller pieces of the Y than had previously been studied. This was slow and frustrating work, because the Y chromosome is full of repetitive sequences and so specific regions are hard to pinpoint. It was 1990 before they found¹ a small coding gene close to the end of the Y chromosome (Fig. 1). Noncommittally they called the gene *SRY*, for sex region on the Y. The final proof that *SRY* was the TDF came from the discovery of *SRY* mutations in XY females⁵ and from the demonstration that adding *Sry* to XX mice was sufficient to induce male development⁶. *SRY* was located on the Y in other placental mammals and, thankfully, even in marsupials⁷.

Researchers in the field imagined that identifying TDF would rapidly lead to an understanding of how it worked, and would point to other genes in the sex-determining pathway. But 25 years on, it has become clear that the pathway kick-started by *SRY* is complex, full of checks and balances.

Initially, *SRY* proved a puzzle because it was unlike any known gene. It turned out to be a member of a previously unidentified family, now called the SOX genes. Painstaking biochemical studies of the *SRY* protein revealed that it bound to a certain DNA sequence and bent it at an angle, presumably to bring other sequences — or the proteins bound to them — into proximity, promoting or inhibiting transcription⁸. The discovery of a different



50 Years Ago

The Royal Society Anniversary Address by Lord Florey, O.M., P.R.S. Perhaps the deployment of Government resources is the modern equivalent of events in the early days of the Society when Fellows contributed—or sometimes did not contribute—a shilling a week towards demonstrating experiments at meetings. There never was enough money... At the moment it is considered to be desirable to give free medicine to all. The application of free calamine lotion to the irritated skins of the populace may be more important than administering to the needs of irritated scientists; but this sort of judgement is in the realm of politics... it has long been the policy of the Society to have symposia and lectures... the popularity of such gatherings has brought difficulties... on one occasion, we had to migrate to the lecture theatre of the Shell Building on the South Bank... one consequence of this peripatetic existence has been that we have had to procure a coffin-like box for the transport of the mace, and I am sure that our original Fellows, and even Charles II himself, might have been somewhat astonished at the adventures of their royal emblem.
From *Nature* 18 December 1965

100 Years Ago

The Romanes Lecture... was a scathing indictment of the ineptitude of the lawyer-politicians who possess a dominating influence on national affairs... To the neglect of science, and the excessive predominance in Parliament and the Government of men with the spirit of the advocate to whom all evidence which will not support their case is unwelcome, Prof. Poulton ascribes the chief mistakes in the conduct of the war.
From *Nature* 22 November 1915